

SEQUENCE LISTING

<110> Xia, Zhi-Qiang
Costa, Michael A
Davlin, Laurence B
Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
Methods of Use

<130> WSUR116430

<140> 09/673,918
<141> 2000-10-23

<150> PCT/US99/08975
<151> 1999-04-23

<150> 60/082,977
<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

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ctt ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc 96
Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu
20 25 30
ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
35 40 45
tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac 192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr
50 55 60
atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp

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aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca				288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala				
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gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca				336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala				
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gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc				384
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys				
	115	120	125	
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Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile				
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Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His				
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gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg				528
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Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro				
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Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn				
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gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt				672
Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly				
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	225	230	235	240
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga				768
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly				
	245	250	255	
ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat				816
Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp				
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Ser				

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Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp	Val	Gln	Asp	Glu
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Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser	Asn	Ser	Thr	Tyr
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Asn	Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met	Phe	Ser	Asn	Ala
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Gly	Ile	Ser	Asp	Pro	Asn	Arg	Pro	Arg	Ile	Ile	Asp	Asn	Glu	Lys	Ala
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Asp	Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly	Val	Phe	Leu	Cys
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Ala	Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Ala	Leu	Thr	Arg	Asn	Leu
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Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn	Cys	Leu	Ser	Pro
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Phe	Gly	Leu	Pro	Thr	Ala	Leu	Gly	Lys	Lys	Phe	Ser	Gly	Ile	Lys	Asn
		195					200					205			
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Pro	Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala	Leu	Tyr	Leu	Ala
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Ser

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Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr	
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aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat	144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp	
35 40 45	
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc	192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser	
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aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa	240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys	
65 70 75 80	
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg	288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	
85 90 95	
ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac	336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp	
100 105 110	
aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga	384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly	
115 120 125	
gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc	432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg	

130	135	140	
agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt			480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly			
145	150	155	160
ggg tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt			528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu			
	165	170	175
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat			576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn			
	180	185	190
tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca			624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser			
	195	200	205
ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga			672
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly			
	210	215	220
aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct			720
Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala			
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ctt tat ctg gct agt gat gag gca aaa tac gtg agt gga cac aat ctg			768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
	245	250	255
ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc			816
Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe			
	260	265	270
caa tat cca gat tct			831
Gln Tyr Pro Asp Ser			
	275		

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 20 25 30
 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
 35 40 45

Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
50 55 60

Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
65 70 75 80

Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
85 90 95

Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
100 105 110

Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
115 120 125

Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
130 135 140

Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
145 150 155 160

Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
165 170 175

Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
180 185 190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
195 200 205

Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
210 215 220

Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
225 230 235 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
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Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
260 265 270

Gln Tyr Pro Asp Ser
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<223> cDNA molecule encoding secoisolariciresinol dehydrogenase wherein
Xaa = any amino acid

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ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc 96
Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
             20             25             30

ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
             35             40             45

tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192
Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
             50             55             60

atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
             65             70             75             80

aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
             85             90             95

gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca 336
Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
             100             105             110

gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt 384
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
             115             120             125

atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata 432
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
             130             135             140

att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat 480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
             145             150             155             160

gct tat tgt ggt gca aaa cat gct gta tta ggc ctt act agg aat ctg 528
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
             165             170             175

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gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct 576
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      180                      185                      190

ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat 624
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
      195                      200                      205

gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt 672
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
      210                      215                      220

aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct 720
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
      225                      230                      235                      240

agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga 768
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
      245                      250                      255

ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac 816
Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
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tct 819
Ser

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<222> (1)..(273)

<223> Secoisolariciresinol dehydrogenase wherein Xaa = any amino acid

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Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
      20                      25                      30

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Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
      35                      40                      45

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Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
      50                      55                      60

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Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp

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Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala						
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Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala						
	100		105			110
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe						
	115		120			125
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile						
	130		135			140
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His						
	145		150		155	160
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu						
		165		170		175
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro						
		180		185		190
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn						
	195		200			205
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly						
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Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala						
	225		230		235	240
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly						
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Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp						
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Ser						

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Gly	Lys	Val	Ala	Leu	Ile	Thr	Gly	Gly	Ala	Ser	Gly	Ile	Gly	Glu	Phe		
			20					25					30				
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Thr	Ala	Lys	Leu	Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp		
		35					40					45					
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Val	Gln	Asp	Glu	Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser		
	50					55					60						
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Asn	Ser	Ile	Tyr	Ile	His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Asp	Val	Lys		
65					70				75						80		
aat	gcc	gtg	gac	aac	aca	ggt	tca	acc	tat	gga	aaa	ctg	gac	att	atg	288	
Asn	Ala	Val	Asp	Asn	Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met		
				85					90					95			
ttc	aac	aat	gca	gga	att	gct	gac	ccc	aac	aag	ccc	cgc	atc	gta	gac	336	
Phe	Asn	Asn	Ala	Gly	Ile	Ala	Asp	Pro	Asn	Lys	Pro	Arg	Ile	Val	Asp		
			100					105					110				
aac	gaa	aaa	gca	gac	ttt	gaa	cgc	ggt	ctc	agc	gta	aat	gta	acc	ggt	384	
Asn	Glu	Lys	Ala	Asp	Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly		
		115					120					125					
ggt	ttc	cta	tgc	atg	aag	cac	gca	gca	cgc	ggt	atg	gtg	cca	gca	cgc	432	
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145					150				155					160			
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Ala	Ala	Ser	His	Ala	Tyr	Cys	Cys	Ser	Lys	His	Ala	Val	Leu	Gly	Leu		
				165					170				175				
act	agg	aat	ctg	gca	gtc	gag	ctc	gga	caa	ttt	ggc	att	agg	ggt	aat	576	
Thr	Arg	Asn	Leu	Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn		
			180					185					190				
tgt	ttg	gct	cct	tac	gcg	ctt	gct	acg	cct	tta	gcc	aag	aaa	ttt	gta	624	
Cys	Leu	Ala	Pro	Tyr	Ala	Leu	Ala	Thr	Pro	Leu	Ala	Lys	Lys	Phe	Val		
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ggg	ctt	gaa	aat	gac	gaa	gat	ttg	gag	aat	gca	atg	agc	ctt	atg	gga	672	
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225	230	235	240
ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg			768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
	245	250	255
ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc			816
Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe			
	260	265	270
caa tat cca gac act			831
Gln Tyr Pro Asp Thr			
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Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser			
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Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys			
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Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met			
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Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp			
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Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly			
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Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg			
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Ala Ala Ser His	Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu					
	165		170		175	
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn						
	180		185		190	
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val						
	195		200		205	
Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly						
	210		215		220	
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala						
225		230		235		240
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu						
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Gln Tyr Pro Asp Thr						
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 <222> (1) .. (828)

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atg gcc act tca cag ctt cga act gca ttc gca aga agg cta gaa gga	48
Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly	
1 5 10 15	
aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca	96
Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr	
20 25 30	
gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc	144
Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val	
35 40 45	
caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat	192
Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn	
50 55 60	

tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat	240
Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn	
65 70 75 80	
gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc	288
Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe	
85 90 95	
aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac	336
Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn	
100 105 110	
gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt	384
Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val	
115 120 125	
ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt	432
Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser	
130 135 140	
ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt	480
Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly	
145 150 155 160	
tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act	528
Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr	
165 170 175	
agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt	576
Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys	
180 185 190	
ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg	624
Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly	
195 200 205	
att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat	672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn	
210 215 220	
ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt	720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu	
225 230 235 240	
ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc	768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe	
245 250 255	
atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa	816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln	
260 265 270	
tat cca gac tct	828

Tyr Pro Asp Ser
275

<210> 10

<211> 276

<212> PRT

<213> Forsythia x intermedia

<400> 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
1 5 10 15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
20 25 30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
35 40 45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
50 55 60

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
65 70 75 80

Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
85 90 95

Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
100 105 110

Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
115 120 125

Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
130 135 140

Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
145 150 155 160

Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
165 170 175

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
180 185 190

Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
195 200 205

Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
210 215 220

Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu

225		230		235		240									
Phe	Leu	Ala	Ser	Asp	Glu	Ala	Gln	Tyr	Val	Ser	Gly	Gln	Asn	Leu	Phe
				245					250					255	
Ile	Asp	Gly	Gly	Phe	Ser	Val	Cys	Asn	Ser	Ala	Ile	Lys	Leu	Phe	Gln
			260					265					270		
Tyr	Pro	Asp	Ser												
			275												

<210> 11
 <211> 21
 <212> PRT
 <213> Forsythia x intermedia

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> N-terminal peptide of F. intermedia
 secoisolariciresinol protein wherein Xaa at
 positions 3, 12 and 20 represents an unidentified
 amino acid residue

<400> 11
 Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
 1 5 10 15
 Ile Thr Gly Xaa Ala
 20

<210> 12
 <211> 17
 <212> PRT
 <213> Forsythia x intermedia

<400> 12
 Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
 1 5 10 15

Lys

<210> 13
 <211> 15
 <212> PRT
 <213> Forsythia x intermedia

<400> 13
 Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys

1 5 10 15

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3, 9, 15 and 18
represents inosine

<400> 14
ggnathggng aracnacngc 20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 15
ccngcrttng araacatdat 20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)

<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 16
ccngcrttnc traacatdat

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer

<400> 17
attccgctag attgcattga

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represent inosine

<400> 18
ccngcrttnc traacatdat

20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaccct cactaaaggg

20

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer

<400> 20
cagcttcgaa ctgcattcgc aag

23

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(22)
<223> T7 PCR primer

<400> 21
cgggatatca ctcagcataa tg

22

<210> 22
<211> 816
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(816)

<400> 22

cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt	48
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu	
1 5 10 15	
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc	96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe	
20 25 30	
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta	144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu	
35 40 45	
ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc	192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile	
50 55 60	
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac	240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn	
65 70 75 80	
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga	288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly	
85 90 95	
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac	336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp	
100 105 110	
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg	384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met	
115 120 125	
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att	432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile	
130 135 140	
tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat gcc	480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala	
145 150 155 160	
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca	528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala	
165 170 175	
gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc	576
Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe	
180 185 190	
ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa	624
Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu	
195 200 205	

gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca 672
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
 210 215 220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt 720
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
 225 230 235 240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg 768
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
 245 250 255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct 816
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
 260 265 270

<210> 23
 <211> 272
 <212> PRT
 <213> Forsythia x intermedia

<400> 23
 Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
 1 5 10 15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
 20 25 30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
 35 40 45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
 50 55 60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
 65 70 75 80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
 85 90 95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
 100 105 110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
 115 120 125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
 130 135 140

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
 145 150 155 160

Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
165 170 175

Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
180 185 190

Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
195 200 205

Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
210 215 220

Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
225 230 235 240

Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
245 250 255

Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
260 265 270

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 24
acatatgcag cttcgaactg cattcgcaag aag

33

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)

<223> PCR primer

<400> 25

catatgggca gacatgttac atgatcaatt gca

33